

SCORE Search Results Details for Application 10552515 and Search Result 20080624_135925_us-10-552-515-1_copy_157_933.szlm.rpr.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_135925_us-10-552-515-1_copy_157_933.szlm.rpr.

[Go Back to previous page](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2008 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2008, 15:38:22 ; Search time 44 Seconds
(without alignments)
1699.101 Million cell updates/sec

Title: US-10-552-515-1_COPY_157_933
Perfect score: 4123
Sequence: 1 QQDVQDGNTTVHYALLSASW.....SELSSHWTPFTVPKASQLQQ 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3429

Minimum DB seq length: 8
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Match	Query Length	DB	ID		Description
1	39	0.9	18	2	A35678		hypothetical prote
2	39	0.9	20	2	PC2248		lambda 112 protein

3	38	0.9	14	1	LFECW	trp operon leader
4	38	0.9	14	2	E90858	trp operon leader
5	38	0.9	14	2	B85761	trp operon leader
6	37	0.9	12	2	S67528	napin - rape (frag
7	37	0.9	15	2	B26997	unspecific monooxy
8	37	0.9	20	2	S29817	cytochrome P450 2C
9	37	0.9	20	2	A33878	myosin light chain
10	37	0.9	20	2	S02002	photosystem II pro
11	37	0.9	20	2	S16202	pyrroline-5-carbox
12	37	0.9	20	2	S53440	glutathione-bindin
13	36	0.9	13	2	S09716	2S albumin large c
14	36	0.9	19	2	B46592	lactase-phlorizin
15	35	0.8	12	2	PH1308	Ig heavy chain DJ
16	35	0.8	19	2	S12268	Qa-2 antigen - mou
17	34	0.8	11	2	D41946	T-cell receptor ga
18	34	0.8	13	2	S14316	photosystem I 9K c
19	34	0.8	17	1	GMSH	gastrin - sheep
20	34	0.8	17	2	A60071	gastrin - rhesus m
21	34	0.8	19	2	S32548	glutathione transf
22	34	0.8	20	2	S56756	link protein - rat
23	33.5	0.8	18	2	A59137	protein Pil - gold
24	33	0.8	15	2	PQ0192	stylar glycoprotei
25	33	0.8	15	2	PQ0073	T-cell receptor be
26	33	0.8	15	2	S08301	epidermal growth f
27	33	0.8	18	2	T03799	leader peptide trp
28	33	0.8	20	2	B39108	lipoprotein AcfD p
29	32.5	0.8	19	2	S60110	hypothetical prote
30	32	0.8	14	1	LFEBWC	trp operon leader
31	32	0.8	14	1	LFEBWT	trp operon leader
32	32	0.8	14	2	S17766	beta-glucosidase (
33	32	0.8	15	2	PQ0174	stylar glycoprotei
34	32	0.8	15	2	PQ0175	stylar glycoprotei
35	32	0.8	17	2	PT0234	Ig heavy chain CRD
36	32	0.8	18	2	JP0102	fibrinogen beta ch
37	32	0.8	18	2	S09722	2S albumin small c
38	32	0.8	20	2	A60728	cytochrome P450 3A
39	32	0.8	20	2	PC2347	base nonspecific a
40	32	0.8	20	2	S10680	probable 7-ethoxyc
41	31	0.8	9	2	A61357	phyllocaerulein -
42	31	0.8	10	2	A61337	caerulein - frog (
43	31	0.8	11	2	PH1375	T antigen variant
44	31	0.8	14	2	PH1615	Ig H chain V-D-J r
45	31	0.8	15	2	S59492	formate dehydrogen

ALIGNMENTS

RESULT 1

A35678

hypothetical protein (proenkephalin 5' region) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 09-Jul-2004

C;Accession: A35678

R;Kilpatrick, D.L.; Zinn, S.A.; Fitzgerald, M.; Higuchi, H.; Sabol, S.L.; Meyerhardt, J.
Mol. Cell. Biol. 10, 3717-3726, 1990

A;Title: Transcription of the rat and mouse proenkephalin genes is initiated at distinct

sites in spermatogenic and somatic cells.

A;Reference number: A35678; MUID:90287163; PMID:2355920

A;Accession: A35678

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-18 <KIL>

A;Cross-references: UNIPROT:Q62256; UNIPARC:UPI0000028BA1; GB:M55181; NID:g201032; PIDN:

AAA40127.1; PID:g201033

Query Match 0.9%; Score 39; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 5.1e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 528 SAGASQGPWED 538
|:| |||
Db 2 SSGKQDSPWED 12

RESULT 2

PC2248

lambda 112 protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Sep-1997

C;Accession: PC2248

R;Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Isegawa, Y.; Iwamatsu, A.; Okada, S.

Biochem. Biophys. Res. Commun. 198, 485-491, 1994

A;Title: Krabbe disease: isolation and characterization of a full-length cDNA for human galactocerebrosidase.

A;Reference number: JC2397; MUID:94128088; PMID:8297359

A;Accession: PC2248

A;Molecule type: mRNA

A;Residues: 1-20 <SAK>

A;Cross-references: UNIPARC:UPI000017C28D; DDBJ:D25284

Query Match 0.9%; Score 39; DB 2; Length 20;
Best Local Similarity 58.3%; Pred. No. 5.8e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 277 WAVLLLEYWKRK 288
| || ||| |
Db 8 WINSLLYYWKNK 19

RESULT 3

LFECW

trp operon leader peptide - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004

C;Accession: A03589; S41637; D64874

R;Yanofsky, C.; Platt, T.; Crawford, I.P.; Nichols, B.P.; Christie, G.E.; Horowitz, H.; van Cleemput, M.; Wu, A.M.

Nucleic Acids Res. 9, 6647-6668, 1981

A;Title: The complete nucleotide sequence of the tryptophan operon of Escherichia coli.

A;Reference number: A93746; MUID:82150258; PMID:7038627

A;Accession: A03589

A;Molecule type: DNA

A;Residues: 1-14 <YAN>
A;Cross-references: UNIPROT:P03053; UNIPARC:UPI000012E89C; GB:J01714; GB:M12471; GB:M12472; GB:M24865; GB:M25264; GB:M25593; GB:M59208; NID:g147953; PIDN:AAA57296.1; PID:g147954
R;Ramesh, V.
Nucleic Acids Res. 21, 5485-5488, 1993
A;Title: NMR evidence for the RNA stem-loop structure involved in the transcription attenuation of E.coli trp operon.
A;Reference number: S41637; MUID:94089403; PMID:7505428
A;Accession: S41637
A;Molecule type: DNA
A;Residues: 1-14 <RAM>
A;Cross-references: UNIPARC:UPI000012E89C
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64874
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-14 <BLAT>
A;Cross-references: UNIPARC:UPI000012E89C; GB:AE000224; GB:U00096; NID:g1787509; PIDN:AAC74347.1; PID:g1787519; UWGP:b1265
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: trpL; trpEe
A;Map position: 27 min
C;Function:
A;Description: involved in control of tryptophan operon transcription by attenuation
C;Superfamily: trp leader peptide

Query Match	0.9%;	Score 38;	DB 1;	Length 14;
Best Local Similarity	83.3%;	Pred. No. 4.5e+03;		
Matches	5;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;

Qy	509	LKGWWQ	514
		:	
Db	7	LKGWWR	12

RESULT 4
E90858
trp operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E90858
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90858

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-14 <HAY>
A;Cross-references: UNIPROT:P03053; UNIPARC:UPI000012E89C; GB:BA000007; PIDN:BAB35260.1;
PID:g13361302; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1837
C;Superfamily: trp leader peptide

Query Match 0.9%; Score 38; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 509 LKGWWQ 514
|||||:
Db 7 LKGWWR 12

RESULT 5

B85761
trp operon leader peptide [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85761
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.
F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin,
A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.;
Blattner, F.R.
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-14 <STO>
A;Cross-references: UNIPROT:P03053; UNIPARC:UPI000012E89C; GB:AE005174; NID:g12515532; PIDN:
AAG56550.1; GSPDB:GN00145; UWGP:Z2545
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: trpL
C;Superfamily: trp leader peptide

Query Match 0.9%; Score 38; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 509 LKGWWQ 514
|||||:
Db 7 LKGWWR 12

RESULT 6

S67528
napin - rape (fragments)
C;Species: Brassica napus (rape)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S67528
 R;Muren, E.; Ek, B.; Rask, L.
 Eur. J. Biochem. 227, 316-321, 1995
 A;Title: Processing of the 2S storage protein pronapin in Brassica napus and in transformed tobacco.
 A;Reference number: S67528; MUID:95154306; PMID:7851402
 A;Accession: S67528
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-6;7-12 <MUR>
 A;Cross-references: UNIPARC:UPI000017B02B; UNIPARC:UPI000017B02C

Query Match 0.9%; Score 37; DB 2; Length 12;
 Best Local Similarity 63.6%; Pred. No. 4.5e+03;
 Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

Qy 140 GPFKTPPEGPQ 150
 |||: |:|||
 Db 3 GPFR--PQGPQ 11

RESULT 7

B26997
 unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2A1, hepatic - rat (fragment)
 N;Alternate names: cytochrome P450a
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C;Accession: B26997
 R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
 Biochemistry 26, 3887-3894, 1987
 A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-carbonitrile-inducible cytochrome P-450 isozymes in rat liver microsomes.
 A;Reference number: A26997; MUID:88000604; PMID:3651420
 A;Accession: B26997
 A;Molecule type: protein
 A;Residues: 1-15 <GRA>
 A;Cross-references: UNIPROT:Q7M0C2; UNIPARC:UPI0000174D45
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane protein

Query Match 0.9%; Score 37; DB 2; Length 15;
 Best Local Similarity 58.3%; Pred. No. 6e+03;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 274 MALWAVLLLEYW 285
 | | : |:||||
 Db 1 MDLASALVLEYW 12

RESULT 8

S29817
 cytochrome P450 2C23 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
 C;Accession: S29817

R;Marie, S.; Roussel, F.; Cresteil, T.
 Biochim. Biophys. Acta 1172, 124-130, 1993
 A;Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
 A;Reference number: S29817; MUID:93176794; PMID:7679925
 A;Accession: S29817
 A;Molecule type: mRNA
 A;Residues: 1-20 <MAR>
 A;Cross-references: UNIPARC:UPI00000E77D7
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; transmembrane protein

Query Match 0.9%; Score 37; DB 2; Length 20;
 Best Local Similarity 53.8%; Pred. No. 8.6e+03;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 708 VGRLLDLLVPDIP 720
 :| ||:| : |||
 Db 8 IGNLLELNLKDIP 20

RESULT 9

A33878
 myosin light chain kinase, smooth muscle - turkey (fragment)
 C;Species: Meleagris gallopavo (common turkey)
 C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
 C;Accession: A33878
 R;Ikebe, M.; Maruta, S.; Reardon, S.
 J. Biol. Chem. 264, 6967-6971, 1989
 A;Title: Location of the inhibitory region of smooth muscle myosin light chain kinase.
 A;Reference number: A33878; MUID:89214114; PMID:2708351
 A;Accession: A33878
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <IKE>
 A;Cross-references: UNIPROT:Q7LZH3; UNIPARC:UPI00001755EC
 C;Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homology;
 immunoglobulin homology; protein kinase homology
 C;Keywords: smooth muscle

Query Match 0.9%; Score 37; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 8.6e+03;
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 143 KTPPEGPQAPRLNQ 156
 ||||: |:: |
 Db 6 KTPPKAATPPQITQ 19

RESULT 10

S02002
 photosystem II protein psbI - spinach chloroplast (tentative sequence) (fragment)
 N;Alternate names: photosystem II 4.8K protein
 C;Species: chloroplast Spinacia oleracea (spinach)
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
 C;Accession: S02002
 R;Ikeuchi, M.; Inoue, Y.
 FEBS Lett. 241, 99-104, 1988

A;Title: A new photosystem II reaction center component (4.8 kDa protein) encoded by chloroplast genome.
A;Reference number: S02002; MUID:89065114; PMID:3058517
A;Accession: S02002
A;Molecule type: protein
A;Residues: 1-20 <IKE>
A;Cross-references: UNIPARC:UPI0000178141
C;Genetics:
A;Gene: psbI
A;Genome: chloroplast
C;Superfamily: photosystem II protein psbI
C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II; thylakoid

Query Match 0.9%; Score 37; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 8.6e+03;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 432 TLKVFIFQFVNIFYSS 446
|||:|:: | |: |
Db 3 TLKLFVYTVVIFVVS 17

RESULT 11

S16202
pyrroline-5-carboxylate reductase - soybean chloroplast
C;Species: chloroplast Glycine max (soybean)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C;Accession: S16202
R;Chilson, O.P.; Kelly-Chilson, A.E.; Siegel, N.R.
Arch. Biochem. Biophys. 288, 350-357, 1991
A;Title: Pyrroline-5-carboxylate reductase in soybean nodules: isolation/partial primary structure/evidence for isozymes.
A;Reference number: S16202; MUID:91378472; PMID:1898034
A;Accession: S16202
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <ARC>
A;Cross-references: UNIPARC:UPI000017B052
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 0.9%; Score 37; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 8.6e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 530 GASQGPWEDD 539
|::| |::|
Db 5 GKAEGQWKDD 14

RESULT 12

S53440
glutathione-binding protein GST1 - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S53440
R;Fitzpatrick, P.J.; Krag, T.O.B.; Hojrup, P.; Sheehan, D.
Biochem. J. 305, 145-150, 1995
A;Title: Characterization of a glutathione S-transferase and a related glutathione-binding protein from gill of the blue mussel, *Mytilus edulis*.
A;Reference number: S53440; MUID:95126896; PMID:7826322
A;Accession: S53440
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <FIT>
A;Cross-references: UNIPROT:Q7M4A5; UNIPARC:UPI000017BDB7

Query Match 0.9%; Score 37; DB 2; Length 20;
Best Local Similarity 58.3%; Pred. No. 8.6e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 331 YFPERSRARRML 342
| | | | | | | :
Db 5 YFPVRGRAEAMV 16

RESULT 13
S09716
2S albumin large chain (1 and 2) nII - rape (fragments)
N;Alternate names: 2S albumin large chain nIII
C;Species: Brassica napus (rape)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C;Accession: S09716; S09718; S09717
R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A;Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins.
A;Reference number: S09720; MUID:90242974; PMID:2185951
A;Accession: S09716
A;Molecule type: protein
A;Residues: 1-9;10-13 <MON>
A;Cross-references: UNIPARC:UPI000017B01F; UNIPARC:UPI000017B020
A;Experimental source: seed
A;Note: 3-Ser was also found
A;Accession: S09718
A;Molecule type: protein
A;Residues: 1-9;10-13 <MO2>
A;Cross-references: UNIPARC:UPI000017B01F; UNIPARC:UPI000017B020
A;Experimental source: seed
A;Accession: S09717
A;Molecule type: protein
A;Residues: 1-9;10-13 <MO3>
A;Cross-references: UNIPARC:UPI000017B01F; UNIPARC:UPI000017B020
A;Experimental source: seed

Query Match 0.9%; Score 36; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 6.1e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 140 GPFKTPPEGP 149
| | : | | | |
Db 3 GPQQRPPPGP 12

RESULT 14

B46592

lactase-phlorizin hydrolase 140K isoform - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Nov-1996

C;Accession: B46592

R;Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.; Rosenberger, J.; Perkinson, J.S.; Cook, G.; Reeds, P.J.

J. Biol. Chem. 268, 13609-13616, 1993

A;Title: In vivo sucrase-isomaltase and lactase-phlorizin hydrolase turnover in the fed adult rat.

A;Reference number: A46592; MUID:93293888; PMID:8514793

A;Accession: B46592

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <DUD>

A;Cross-references: UNIPARC:UPI00000E82F3

A;Note: sequence extracted from NCBI backbone (NCBIP:134560)

C;Keywords: carbohydrate digestion; intestine

Query Match	0.9%;	Score 36;	DB 2;	Length 19;
Best Local Similarity	54.5%;	Pred. No. 9.8e+03;		
Matches	6;	Conservative	2;	Mismatches 3; Indels 0; Gaps 0;

Qy 506 IPKLKGWWQKF 516

:|| | |:||

Db 9 VPKAKIVWEKF 19

RESULT 15

PH1308

Ig heavy chain DJ region (clone C731-94) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1308

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G. J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoblastic leukemia as evidence for an in utero transforming event.

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1308

A;Molecule type: DNA

A;Residues: 1-12 <WAS>

A;Cross-references: UNIPARC:UPI000017C24B

C;Keywords: heterotetramer; immunoglobulin

Query Match	0.8%;	Score 35;	DB 2;	Length 12;
Best Local Similarity	80.0%;	Pred. No. 6.7e+03;		
Matches	4;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;

Qy 167 WGKWN 171

||:||

Db 7 WGQWN 11

Search completed: June 24, 2008, 15:47:36

Job time : 47 secs

SCORE 2.0